



IFWO

## RAW SEQUENCE LISTING

DATE: 07/29/2004

PATENT APPLICATION: US/10/721,922A

TIME: 09:40:12

Input Set : D:\seqlistcorrected2.txt

Output Set: N:\CRF4\07292004\J721922A.raw

3 <110> APPLICANT: Pompejus, Markus  
4 Kroger, Burkhard  
5 Schroder, Hartwig  
6 Zelder, Oskar  
7 Haberhauer, Gregor  
9 <120> TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
10 INVOLVED IN HOMEOSTASIS AND ADAPTATION  
12 <130> FILE REFERENCE: BGI-132CPCN  
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/721,922A  
C--> 14 <141> CURRENT FILING DATE: 2003-11-24  
14 <150> PRIOR APPLICATION NUMBER: 09/6027777  
15 <151> PRIOR FILING DATE: 2000-02-23  
17 <150> PRIOR APPLICATION NUMBER: 09/603124  
18 <151> PRIOR FILING DATE: 2000-06-23  
20 <150> PRIOR APPLICATION NUMBER: US 60/141031  
21 <151> PRIOR FILING DATE: 1999-06-25  
23 <150> PRIOR APPLICATION NUMBER: US 60/143694  
24 <151> PRIOR FILING DATE: 1999-07-14  
26 <150> PRIOR APPLICATION NUMBER: US 60/151778  
27 <151> PRIOR FILING DATE: 1999-08-31  
29 <150> PRIOR APPLICATION NUMBER: DE 19931418.7  
30 <151> PRIOR FILING DATE: 1999-07-08  
32 <150> PRIOR APPLICATION NUMBER: DE 19932124.8  
33 <151> PRIOR FILING DATE: 1999-07-09  
35 <150> PRIOR APPLICATION NUMBER: DE 19932126.4  
36 <151> PRIOR FILING DATE: 1999-07-09  
38 <150> PRIOR APPLICATION NUMBER: DE 19932127.2  
39 <151> PRIOR FILING DATE: 1999-07-09  
41 <150> PRIOR APPLICATION NUMBER: DE 19932133.7  
42 <151> PRIOR FILING DATE: 1999-07-09  
44 <150> PRIOR APPLICATION NUMBER: DE 19932207.4  
45 <151> PRIOR FILING DATE: 1999-07-09  
47 <150> PRIOR APPLICATION NUMBER: DE 19932208.2  
48 <151> PRIOR FILING DATE: 1999-07-09  
50 <150> PRIOR APPLICATION NUMBER: DE 19932225.2  
51 <151> PRIOR FILING DATE: 1999-07-09  
53 <150> PRIOR APPLICATION NUMBER: DE 19932229.5  
54 <151> PRIOR FILING DATE: 1999-07-09  
56 <150> PRIOR APPLICATION NUMBER: DE 19932914.1  
57 <151> PRIOR FILING DATE: 1999-07-14  
59 <150> PRIOR APPLICATION NUMBER: DE 19933006.9  
60 <151> PRIOR FILING DATE: 1999-07-14  
62 <150> PRIOR APPLICATION NUMBER: DE 19940765.7

(pg. 6)

**ENTERED**

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63 <151> PRIOR FILING DATE: 1999-08-27
65 <150> PRIOR APPLICATION NUMBER: DE 19940768.1
66 <151> PRIOR FILING DATE: 1999-08-27
68 <150> PRIOR APPLICATION NUMBER: DE 19940831.9
69 <151> PRIOR FILING DATE: 1999-08-27
71 <150> PRIOR APPLICATION NUMBER: DE 19940832.7
72 <151> PRIOR FILING DATE: 1999-08-27
74 <150> PRIOR APPLICATION NUMBER: DE 19941385.1
75 <151> PRIOR FILING DATE: 1999-08-31
77 <150> PRIOR APPLICATION NUMBER: DE 19941396.7
78 <151> PRIOR FILING DATE: 1999-08-31
80 <150> PRIOR APPLICATION NUMBER: DE 19942087.4
81 <151> PRIOR FILING DATE: 1999-09-03
83 <160> NUMBER OF SEQ ID NOS: 480
85 <210> SEQ ID NO: 1
86 <211> LENGTH: 1581
87 <212> TYPE: DNA
88 <213> ORGANISM: Corynebacterium glutamicum
90 <220> FEATURE:
91 <221> NAME/KEY: CDS
92 <222> LOCATION: (101)..(1558)
93 <223> OTHER INFORMATION: RXA02702
95 <400> SEQUENCE: 1
96 gcaggtaacg cctccacggt gattgcagac atgattgctg caactatcaa tagccaacac 60
98 aactaaaacg accagctcaa cgcaaaggaa tagtttaaag gtg acc act cca cac 115
99                                     Val Thr Thr Pro His
100                                     1      5
102 ttg gat tct gca caa gat att gat ctg tcc cgc gtc cac ctc atc ggt 163
103 Leu Asp Ser Ala Gln Asp Ile Asp Leu Ser Arg Val His Leu Ile Gly
104                                     10      15      20
106 att ggc gga gcc gga atg tct ggc gtt gcc cga atc ctg ctt gcc cgc 211
107 Ile Gly Gly Ala Gly Met Ser Gly Val Ala Arg Ile Leu Leu Ala Arg
108                                     25      30      35
110 ggt aag aca gtc act ggt tcc gat gcc aaa gat tcc cgc acc ttg ctt 259
111 Gly Lys Thr Val Thr Gly Ser Asp Ala Lys Asp Ser Arg Thr Leu Leu
112                                     40      45      50
114 cca ctc cgc gcc gtg gga gcc acc atc gca gtg gga cac gct gcg gaa 307
115 Pro Leu Arg Ala Val Gly Ala Thr Ile Ala Val Gly His Ala Ala Glu
116                                     55      60      65
118 aac ctt gag ctt tcc ggc gaa ctt ccc acc gtc gtg gtg acc tct ttt 355
119 Asn Leu Glu Leu Ser Gly Glu Leu Pro Thr Val Val Val Thr Ser Phe
120 70                                     75      80      85
122 gcc gcc att ccg caa gac aac ccg gaa ctt gtt cgt gca cgt gaa gaa 403
123 Ala Ala Ile Pro Gln Asp Asn Pro Glu Leu Val Arg Ala Arg Glu Glu
124                                     90      95      100
126 ggc att ccg gtt att cgt cgc tcc gat ctg ttg ggc gaa ttg ctg gaa 451
127 Gly Ile Pro Val Ile Arg Arg Ser Asp Leu Leu Gly Glu Leu Leu Glu
128                                     105      110      115
130 ggc tcc acc cag gtc ttg atc gcg ggt acc cac ggt aag acc tcc acc 499

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131	Gly	Ser	Thr	Gln	Val	Leu	Ile	Ala	Gly	Thr	His	Gly	Lys	Thr	Ser	Thr	
132			120					125					130				
134	acc	tct	atg	tct	gtg	gta	gct	atg	cag	gca	gcg	ggc	atg	gat	cca	agc	547
135	Thr	Ser	Met	Ser	Val	Val	Ala	Met	Gln	Ala	Ala	Gly	Met	Asp	Pro	Ser	
136		135					140					145					
138	ttt	gct	atc	ggc	gga	cag	ctc	aac	aag	gct	ggc	acc	aat	gcg	cac	cat	595
139	Phe	Ala	Ile	Gly	Gly	Gln	Leu	Asn	Lys	Ala	Gly	Thr	Asn	Ala	His	His	
140	150					155					160				165		
142	gga	act	ggt	gag	gtc	ttt	atc	gct	gaa	gca	gat	gaa	tct	gac	gca	tcg	643
143	Gly	Thr	Gly	Glu	Val	Phe	Ile	Ala	Glu	Ala	Asp	Glu	Ser	Asp	Ala	Ser	
144				170						175					180		
146	ctg	ctg	cgc	tac	aag	cca	aat	gtt	gca	gtg	gtc	acc	aat	gtg	gaa	cca	691
147	Leu	Leu	Arg	Tyr	Lys	Pro	Asn	Val	Ala	Val	Val	Thr	Asn	Val	Glu	Pro	
148			185					190					195				
150	gac	cac	ctg	gac	ttc	ttt	aaa	acc	cct	gaa	gcc	tac	ttc	caa	gtg	ttc	739
151	Asp	His	Leu	Asp	Phe	Phe	Lys	Thr	Pro	Glu	Ala	Tyr	Phe	Gln	Val	Phe	
152			200					205					210				
154	gac	gat	ttc	gca	gga	cgc	atc	acc	ccg	aac	ggc	aag	ctg	gtt	gtg	tgc	787
155	Asp	Asp	Phe	Ala	Gly	Arg	Ile	Thr	Pro	Asn	Gly	Lys	Leu	Val	Val	Cys	
156		215				220					225						
158	ctg	aac	gat	cct	cac	gca	gcg	gag	ctg	ggg	gag	agg	tct	gtc	cgc	aag	835
159	Leu	Asn	Asp	Pro	His	Ala	Ala	Glu	Leu	Gly	Glu	Arg	Ser	Val	Arg	Lys	
160	230				235					240					245		
162	ggt	atc	aag	act	gtt	ggt	tac	ggt	acc	gct	gac	gcc	gta	cag	gca	cac	883
163	Gly	Ile	Lys	Thr	Val	Gly	Tyr	Gly	Thr	Ala	Asp	Ala	Val	Gln	Ala	His	
164				250				255						260			
166	cct	gag	gtt	cca	gcg	atg	gct	acc	atc	gtg	gat	tcc	caa	gtt	gtc	gca	931
167	Pro	Glu	Val	Pro	Ala	Met	Ala	Thr	Ile	Val	Asp	Ser	Gln	Val	Val	Ala	
168			265					270					275				
170	gaa	ggc	acc	cgc	gcc	acc	atc	aac	atc	gat	gga	cag	gaa	gta	tct	gtg	979
171	Glu	Gly	Thr	Arg	Ala	Thr	Ile	Asn	Ile	Asp	Gly	Gln	Glu	Val	Ser	Val	
172			280					285					290				
174	att	ctt	caa	atc	cct	ggt	gat	cac	atg	gta	ctc	aac	ggt	gca	gcc	gcc	1027
175	Ile	Leu	Gln	Ile	Pro	Gly	Asp	His	Met	Val	Leu	Asn	Gly	Ala	Ala	Ala	
176		295				300						305					
178	ctg	ctg	gcc	gga	tac	ctg	gtg	ggt	ggg	gac	gtc	gac	aag	ctt	gtt	gaa	1075
179	Leu	Leu	Ala	Gly	Tyr	Leu	Val	Gly	Gly	Asp	Val	Asp	Lys	Leu	Val	Glu	
180	310				315					320					325		
182	ggc	ttg	tcg	gat	ttc	tcc	ggc	gtg	cga	cgc	cgc	ttt	gag	ttc	cac	ggt	1123
183	Gly	Leu	Ser	Asp	Phe	Ser	Gly	Val	Arg	Arg	Arg	Phe	Glu	Phe	His	Gly	
184				330				335					340				
186	gct	atc	gag	ggc	ggc	aaa	ttt	aat	ggc	gct	gct	att	tat	gat	gat	tac	1171
187	Ala	Ile	Glu	Gly	Gly	Lys	Phe	Asn	Gly	Ala	Ala	Ile	Tyr	Asp	Asp	Tyr	
188			345					350					355				
190	gca	cac	cac	cca	acg	gaa	gta	act	gca	gtg	ctc	agc	gct	gcg	cgc	acc	1219
191	Ala	His	His	Pro	Thr	Glu	Val	Thr	Ala	Val	Leu	Ser	Ala	Ala	Arg	Thr	
192			360					365					370				
194	cgg	gtg	aag	gcc	gct	gga	aag	ggc	cgt	gtc	atc	gtc	gcg	ttc	caa	cca	1267
195	Arg	Val	Lys	Ala	Ala	Gly	Lys	Gly	Arg	Val	Ile	Val	Ala	Phe	Gln	Pro	

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196      375      380      385
198 cat tta tac tca cgc acc ata gaa ttc caa aag gag ttc gcg ggg gca 1315
199 His Leu Tyr Ser Arg Thr Ile Glu Phe Gln Lys Glu Phe Ala Gly Ala
200 390      395      400      405
202 ctg tca ctg gca gac gct gcc gtg gtg ctt gag att tac gga gcg cgc 1363
203 Leu Ser Leu Ala Asp Ala Ala Val Val Leu Glu Ile Tyr Gly Ala Arg
204      410      415      420
206 gaa caa ccg gtg gat ggc gtg tcc tcg gaa atc atc acc gat gcg atg 1411
207 Glu Gln Pro Val Asp Gly Val Ser Ser Glu Ile Ile Thr Asp Ala Met
208      425      430      435
210 acc att cca gtg gtg tac gaa cct aat ttc tct gca gtc cca gaa cgc 1459
211 Thr Ile Pro Val Val Tyr Glu Pro Asn Phe Ser Ala Val Pro Glu Arg
212      440      445      450
214 att gca gaa atc gca gga cct aat gac atc gtg ctc acc atg ggt gca 1507
215 Ile Ala Glu Ile Ala Gly Pro Asn Asp Ile Val Leu Thr Met Gly Ala
216      455      460      465
218 ggt tcc gtg acc atg ctt gct cca gaa atc ctg gat cag ctg caa aac 1555
219 Gly Ser Val Thr Met Leu Ala Pro Glu Ile Leu Asp Gln Leu Gln Asn
220 470      475      480      485
222 aat taggacgtaa gtgaacaagg cag 1581
223 Asn
227 <210> SEQ ID NO: 2
228 <211> LENGTH: 486
229 <212> TYPE: PRT
230 <213> ORGANISM: Corynebacterium glutamicum
232 <400> SEQUENCE: 2
233 Val Thr Thr Pro His Leu Asp Ser Ala Gln Asp Ile Asp Leu Ser Arg
234 1 5 10 15
236 Val His Leu Ile Gly Ile Gly Gly Ala Gly Met Ser Gly Val Ala Arg
237 20 25 30
239 Ile Leu Leu Ala Arg Gly Lys Thr Val Thr Gly Ser Asp Ala Lys Asp
240 35 40 45
242 Ser Arg Thr Leu Leu Pro Leu Arg Ala Val Gly Ala Thr Ile Ala Val
243 50 55 60
245 Gly His Ala Ala Glu Asn Leu Glu Leu Ser Gly Glu Leu Pro Thr Val
246 65 70 75 80
248 Val Val Thr Ser Phe Ala Ala Ile Pro Gln Asp Asn Pro Glu Leu Val
249 85 90 95
251 Arg Ala Arg Glu Glu Gly Ile Pro Val Ile Arg Arg Ser Asp Leu Leu
252 100 105 110
254 Gly Glu Leu Leu Glu Gly Ser Thr Gln Val Leu Ile Ala Gly Thr His
255 115 120 125
257 Gly Lys Thr Ser Thr Thr Ser Met Ser Val Val Ala Met Gln Ala Ala
258 130 135 140
260 Gly Met Asp Pro Ser Phe Ala Ile Gly Gly Gln Leu Asn Lys Ala Gly
261 145 150 155 160
263 Thr Asn Ala His His Gly Thr Gly Glu Val Phe Ile Ala Glu Ala Asp
264 165 170 175
266 Glu Ser Asp Ala Ser Leu Leu Arg Tyr Lys Pro Asn Val Ala Val Val

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267          180          185          190
269 Thr Asn Val Glu Pro Asp His Leu Asp Phe Phe Lys Thr Pro Glu Ala
270          195          200          205
272 Tyr Phe Gln Val Phe Asp Asp Phe Ala Gly Arg Ile Thr Pro Asn Gly
273          210          215          220
275 Lys Leu Val Val Cys Leu Asn Asp Pro His Ala Ala Glu Leu Gly Glu
276 225          230          235          240
278 Arg Ser Val Arg Lys Gly Ile Lys Thr Val Gly Tyr Gly Thr Ala Asp
279          245          250          255
281 Ala Val Gln Ala His Pro Glu Val Pro Ala Met Ala Thr Ile Val Asp
282          260          265          270
284 Ser Gln Val Val Ala Glu Gly Thr Arg Ala Thr Ile Asn Ile Asp Gly
285          275          280          285
287 Gln Glu Val Ser Val Ile Leu Gln Ile Pro Gly Asp His Met Val Leu
288          290          295          300
290 Asn Gly Ala Ala Ala Leu Leu Ala Gly Tyr Leu Val Gly Gly Asp Val
291 305          310          315          320
293 Asp Lys Leu Val Glu Gly Leu Ser Asp Phe Ser Gly Val Arg Arg Arg
294          325          330          335
296 Phe Glu Phe His Gly Ala Ile Glu Gly Gly Lys Phe Asn Gly Ala Ala
297          340          345          350
299 Ile Tyr Asp Asp Tyr Ala His His Pro Thr Glu Val Thr Ala Val Leu
300          355          360          365
302 Ser Ala Ala Arg Thr Arg Val Lys Ala Ala Gly Lys Gly Arg Val Ile
303          370          375          380
305 Val Ala Phe Gln Pro His Leu Tyr Ser Arg Thr Ile Glu Phe Gln Lys
306 385          390          395          400
308 Glu Phe Ala Gly Ala Leu Ser Leu Ala Asp Ala Ala Val Val Leu Glu
309          405          410          415
311 Ile Tyr Gly Ala Arg Glu Gln Pro Val Asp Gly Val Ser Ser Glu Ile
312          420          425          430
314 Ile Thr Asp Ala Met Thr Ile Pro Val Val Tyr Glu Pro Asn Phe Ser
315          435          440          445
317 Ala Val Pro Glu Arg Ile Ala Glu Ile Ala Gly Pro Asn Asp Ile Val
318          450          455          460
320 Leu Thr Met Gly Ala Gly Ser Val Thr Met Leu Ala Pro Glu Ile Leu
321 465          470          475          480
323 Asp Gln Leu Gln Asn Asn
324          485
327 <210> SEQ ID NO: 3
328 <211> LENGTH: 1539
329 <212> TYPE: DNA
330 <213> ORGANISM: Corynebacterium glutamicum
332 <220> FEATURE:
333 <221> NAME/KEY: CDS
334 <222> LOCATION: (101)..(1516)
335 <223> OTHER INFORMATION: RXA02705
337 <400> SEQUENCE: 3
338 cgtgaccatc cgtttctggc tgatcgcgat catggctgtg ttggcgggtg tcggtgtgtt 60

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RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 07/29/2004  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:315; N Pos. 658

Seq#:387; N Pos. 71

Seq#:425; N Pos. 350,354,355,364,367

Seq#:427; N Pos. 11,12,14,17,24,28,29,62,88,91,97

**VERIFICATION SUMMARY**

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No  
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:29135 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:315 after pos.:643  
L:34118 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:387 after pos.:50  
L:37094 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:425 after pos.:349  
L:37137 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:427 after pos.:0  
L:37139 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:427 after pos.:60